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## OM protein - protein search, using sw model

Run on: June 27, 2003, 18:11:16 ; Search time 40 Seconds

(without alignments)  
853.193 Million cell updates/sec

Title: US-09-922-895-1

Perfect score: 1854  
Sequence: 1 MTSLSDFVEFGTSTYDDV.....LERTSSVSPSTAPELSYR 355Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1851	99.8	355	2	G02436
2	1240	66.9	359	2	I49341
3	1181.5	63.7	355	2	A45177
4	1117.5	60.3	355	2	I49339
5	958.5	51.7	383	2	S55594
6	947	51.1	360	2	JC2443
7	938.5	50.6	352	2	A43113
8	927.5	50.0	356	2	I49340
9	886.5	47.8	374	2	I38450
10	803.5	43.3	360	2	A57160
11	780.5	42.1	360	2	JC4587
12	710.5	38.3	354	2	I58186
13	692.5	37.4	355	2	JC5067
14	684	36.9	355	2	JC4304
15	659.5	35.6	344	2	JC5942
16	572	30.9	369	2	JC5068
17	541.5	29.2	378	2	B55735
18	527.5	28.5	378	2	A45680
19	524.5	28.3	367	2	JE0349
20	521	28.1	333	2	I65989
21	515	27.8	378	2	A55735
22	508	27.4	352	2	A45747
23	503	27.1	352	2	G00048
24	503	27.1	360	2	A53611
25	502	27.1	353	2	S28787
26	491.5	26.5	355	2	J01231
27	484.5	26.1	359	2	A42656
28	481.5	26.0	350	2	A39445
29	480.5	25.9	350	2	JN0621

30	478.5	25.8	358	2	A53752	interleukin-8 rece
31	478	25.8	359	2	JC2134	angiotensin II rec
32	476	25.7	359	2	S44425	angiotensin II rec
33	474.5	25.6	359	2	J01516	angiotensin II rec
34	472	25.5	359	2	JH0621	angiotensin II rec
35	469	25.3	359	2	S15403	angiotensin II rec
36	466	25.1	362	2	JN0694	angiotensin II rec
37	465.5	25.1	359	2	JC1104	angiotensin II rec
38	465	25.1	359	2	A48857	angiotensin II rec
39	458.5	24.7	374	2	S42628	G protein-coupled
40	457.5	24.7	359	2	JC1194	angiotensin II rec
41	457	24.6	359	2	I51372	angiotensin II rec
42	454.5	24.5	359	2	I39418	angiotensin II rec
43	452.5	24.4	374	2	S32785	G protein-coupled
44	450	24.3	372	2	S26667	G protein-coupled
45	442.5	23.9	327	2	S56162	MCGR5 protein - h

## ALIGNMENTS

## RESULT 1

G02436

Chemokine (C-C) receptor 3 - human

N/Alternate names: C-C CKR-3

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 04-Mar-2000

C/Accession: G02436; A57237

R/Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A/Reference number: H01272

A/Accession: G02436

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-355 &lt;POND&gt;

A/Cross-references: EMBL:U49727; NID:91477560; PIDN:AMB09726.1; PID:91477561

R/Combadlere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A/Title: Cloning and functional expression of a human eosinophil CC chemokine recepto

A/Reference number: A57237; MUID:95348056; PMID:7652448

A/Accession: A57237

A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 &lt;CON&gt;

A/Cross-references: GB:U28694; NID:91199579; PIDN:AAC50469.1; PID:91199580

A/Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC504

C/Genetics:

A/Gene: GDB:CKR3

A/Cross-references: GDB:579624; OMIM:601268

A/Map position: 3p21-3p21

C/Superfamily: vertebrate rhodopsin

Oy	1	MTSLSDFVEFGTSTYDDVGLCEKADTRALMAQFVPLSLVFTVGLGNVVVMIIL	60
Db	1	MTSLSDFVEFGTSTYDDVGLCEKADTRALMAQFVPLSLVFTVGLGNVVVMIIL	60
Oy	61	KYRRLRIMTNLYILNLAIISDLFLVTLPEFWHYHVGHNWPGHGMCKLLSGFYHTGLXSE	120
Db	61	KYRRLRIMTNLYILNLAIISDLFLVTLPEFWHYHVGHNWPGHGMCKLLSGFYHTGLXSE	120





Db 197 -GMNETHIMNIGLVLPLLMVICYSGILKTLIRCNKRHRRAVIFTIMIVLEF 255  
OY 252 WTPYVAIILSSYOSILEGNCDSRKHDLVMTVEVIASHCCNPIYAFVGRFRY 311  
DB 256 WTPYVAIILMTFOEFPLSNCSSTQDQATQVETIGMHCINPIIYAFVGRFRY 315  
OY 312 LRFHFHRLMLHMGRIYFPLDSEKIER-TSSVSPSTABEUS 352  
DB 316 LSVFRRKHITRFRCKOCFVFEYFVDGYTSTWTPSTGEHVS 357

RESULT 7  
A3113  
Chemokine (C-C) receptor 5 - human  
M:Alternate names: C-C CRF-5; CCR5  
C:Species: Homo sapiens (man)  
C:Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 20-Jun-2000  
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833  
R:Samson, M.; Ladbbe, O.; Molliereau, C.; Vassart, G.; Parmentier, M.  
Biochembiol 35, 3362-3367, 1996  
A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
A:Reference number: S71808; MUID:96241590; PMID:8639485  
A:Accession: A43113  
A:Molecule type: mRNA  
A:Residues: 1-352 <SAML>  
A:Cross-references: GB:X91492; NID:g1262810; PIDN:CA62796.1; PID:g1262811  
R:Samson, M.; Libert, F.; Doznan, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost  
M.; Imali, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa  
Nature 382, 722-725, 1996  
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles C  
A:Reference number: S71808; MUID:96241590; PMID:8639485  
A:Accession: S71808  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 182-206; 207-230 <SAM2>  
A:Accession: A58834  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-184; 'IKRSHGACAPAAACCHGLILGNPKNSASVK' <SAM3>  
A:Cross-references: GB:X93393; NID:g1524062; PIDN:CA67767.1; PID:g1524063  
A:Note: this frameshift mutation results in a non-functional receptor but confers a degra  
nd may have had a selective advantage by conferring resistance to Yersinia plague infect  
R:Combadere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.  
J. Leukoc. Biol. 60, 147-152, 1996  
A:Title: Cloning and functional expression of CC CRF5, a human monocyte CC chemokine rec  
A:Reference number: A58832; MUID:96295970; PMID:8699119  
A:Accession: A58832  
A:Molecule type: mRNA  
A:Residues: 1-352 <COM1>  
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AA617071.1; PID:g1502409  
R:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R:Combadere, C.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: H01541  
A:Accession: G02653  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-89, 'L', '91-352 <COM2>  
A:Cross-references: EMBL:057840  
R:Raport, C.J.; Gosling, J.; Schmelkard, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996  
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine  
A:Reference number: A58833; MUID:96291862; PMID:8663314  
A:Accession: A58833  
A:Molecule type: mRNA  
A:Residues: 1-352 <RAP>  
A:Cross-references: GB:U54994; NID:g1457945; PIDN:AA60598.1; PID:g1457946  
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30374), MIP-1beta (see  
C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine C  
C:Genetics:  
A:Gene: GDB:CMKR5; CCR5; CRF-5; CC-CRF-5; CCR5; ChemR13  
A:Cross-references: GDB:1230510; OMIM:601373  
A:Map position: 3p21-3p21

C:Function:  
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RA  
A:Note: probably acts to control granulocyte proliferation and differentiation  
C:Superfamily: Vertebrate rhodopsin  
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmem  
E/32-56/Domain: transmembrane #status predicted <TM1>  
E/67-87/Domain: transmembrane #status predicted <TM2>  
E/103-124/Domain: transmembrane #status predicted <TM3>  
E/142-166/Domain: transmembrane #status predicted <TM4>  
E/193-218/Domain: transmembrane #status predicted <TM5>  
E/236-257/Domain: transmembrane #status predicted <TM6>  
E/285-300/Domain: transmembrane #status predicted <TM7>  
E/20-269,101-178/Disulfide bonds: #status predicted  
E/268/Binding site: carbohydrate (Asn) (covalent) #status predicted  
E/336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
E/340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 50.6%; Score 927.5; DB 2; Length 352;  
Best Local Similarity 53.3%; Pred. No. 1e-71;  
Matches 177; Conservative 62; Mismatches 90; Indels 3; Gaps 3;

OY 24 CEKADTRALMAQFVPEPLYSIVFTVGLGNVVVMTILRYRLIMTNTILNLASDLLE 83  
DB 20 COKINVKQIAARLPLPLYSIVIFPGVGNMLVILLINCKRKSKTDIYLLNLASDLLE 79  
OY 84 LVTLPFWHYVGNHNVFEGHCKLLSGFYHTGLYSEIFITLLTIDRYLVAIVAFALR 143  
DB 80 LITVPEFMAHYAAQ-CMDGENTMCOLLTGIFGFPFSGIFITLLTIDRYLVAIVAFALR 138  
OY 144 ARTVFEVYTSIVTGLVLAALPEFIFEPFEELEEDLCSALYEDDYVSMRHHHTRM 203  
DB 139 ARTVFEVYTSIVTGLVLAALPEFIFEPFEELEEDLCSALYEDDYVSMRHHHTRM 198  
OY 204 TIFCLVPLPLVNAICYGTGILTKLRCPK-KKKRYKRIILFYMAVFFLFWPYNAVILS 262  
DB 199 VILGVPLPLVNAICYGTGILTKLRCPK-KKKRYKRIILFYMAVFFLFWPYNAVILS 258  
OY 263 STQSLIFGDCRSKRLDLVMTVEVIASHCCNPIYAFVGRFRYRLHFRHILM 322  
DB 259 TFOEFPLSNCSSTQDQATQVETIGMHCINPIIYAFVGRFRYRLHFRHILM 318  
OY 323 HLGRIYFPLDSEKIER-TSSVSPSTABEUS 353  
DB 319 RFCCKCSITQDEAPERASSVYTRSTGEHVS 350

RESULT 8  
I49340  
MIP-1 alpha receptor like-1 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C:Accession: I49340  
R:Guo, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A:Title: Cloning and differential tissue-specific expression of three mouse beta chem  
A:Reference number: I49339; MUID:95340546; PMID:7542241  
A:Accession: I49340  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-356 <RES>  
A:Cross-references: EMBL:028405; NID:g881549; PIDN:AA69154.1; PID:g881550  
C:Superfamily: vertebrate rhodopsin

Query Match 50.0%; Score 927.5; DB 2; Length 356;  
Best Local Similarity 50.7%; Pred. No. 8.6e-71;  
Matches 176; Conservative 68; Mismatches 102; Indels 1; Gaps 1;

OY 7 TVEETGTSYDDV-GLCEKADTRALMAQFVPEPLYSIVFTVGLGNVVVMTILRYRL 65  
DB 7 TEPYNTVAKNDPMGSCFLCFSINVRAGITVPTPLYSIVIFIGVHVLVLLIQHRL 66  
OY 66 RMTNTIYLLNLASDLLEPLVTPFWHYVGNHNVFEGHCKLLSGFYHTGLYSEIFIT 125

Db 67 RNMSTIYLFMAISDLVFLSTLPFWVDYIMKGMIFGNMCKEVSQYVYGLYDMFFIT 126  
QY 126 LITIDRIYLAIVHAFALRARTVGTGVTISVTWGLAVLAALPEFIYETEELFEETLCSA 185  
Db 127 LITIDRIYLAIVHAFALRARTVGTGVTISVTWGLAVLAALPEFIYETEELFEETLCSA 186  
QY 186 LYEEDVYVSRNHEHTLMTFICLVPLLVMAICTGTGIIKTLRCPKSKKKAIRLIVIM 245  
Db 187 ILPRKSLIRFLRCALTMNITGLTLPPLAMICTYTRIIVLHRRPNKKAKAVMLIFVIT 246  
QY 246 AVPEFIEMTPYNAIILSSYSLGNCDSKSHLDVMAIYEVAYSHCCNPIYAFV 305  
Db 247 LTFELLPALPYLAIVSAFEDVETPSCLNSQVDLSMTTEALATYHCCVNPVYVFG 306  
QY 306 EREKRYLHFEHRLHMLGRYIFLPSEKLETSVSPSTAEPELS 352  
Db 307 KRRKRYLMOLFRRHTAITLPQWLPFLSEDAQASALPSTVEIETS 353

## RESULT 9

138450  
chemokine (C-C) receptor 2, splice form A - human  
N:Alternate names: C-C-CCR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence, revision 16-Feb-1996 #text, change 13-Aug-1999  
C:Accession: 138450  
R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins  
A:Reference number: A53477; MUID:94195821; PMID:816186  
A:Accession: 138450  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <RES>  
C:Cross-references: EMBL:003882; NID:9472555; PIDN:AA19119.1; PID:9472556  
C:Genetics:  
A:Gene: GDB:CMKBR2  
A:Cross-references: GDB:337364; OMIM:601267  
A:Map position: 3p21-3p21  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane  
F:44-68/Domain: transmembrane #status predicted <TM1>  
F:79-99/Domain: transmembrane #status predicted <TM2>  
F:115-136/Domain: transmembrane #status predicted <TM3>  
F:154-178/Domain: transmembrane #status predicted <TM4>  
F:208-226/Domain: transmembrane #status predicted <TM5>  
F:244-265/Domain: transmembrane #status predicted <TM6>  
F:292-309/Domain: transmembrane #status predicted <TM7>  
F:314/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:321-327/113-190/Disulfide bonds: #status predicted

Query Match 47.8%; Score 886.5; DB 2; Length 374;  
Best Local Similarity 54.2%; Pred. No. 2, 66-67;  
Matches 166; Conservative 57; Mismatches 72; Indels 11; Gaps 5;

QY 14 TSYID-DVGLCEKADRALMAQFVPPYLSLVFTVGLGNVVMILIKYRRLRIMNIX 72  
Db 21 TTFEDYDYGAPCHRFVDVKQJGALPLPYLSLVFTFVGNNLVLLINCKKLCIDIX 80  
QY 73 LNMALISDLFLVTLPMVHVRGNHNVFGHCKLLSGFHTGLYSIFILLITIDRY 132  
Db 81 LNMALISDLFLVTLPMVHVRGNHNVFGHCKLLSGFHTGLYSIFILLITIDRY 139  
QY 133 LAIVHAFALRARTVGTGVTISVTWGLAVLAALPEFIYETEELFEETLCSALYEDTV 192  
Db 140 LAIVHAFALRARTVGTGVTISVTWGLAVLAALPEFIYETEELFEETLCSALYEDTV 196  
QY 193 YSMRHFPLRMFTFICLVPLLVMAICTGTGIIKTLRCPKSKKKAIRLIVIM 251  
Db 197 -GMNFTIMRNITGLVPLLVMAICTGTGIIKTLRCPKSKKKAIRLIVIM 255  
QY 252 WTPFNVAIILSSYSLGNCDSKSHLDVMAIYEVAYSHCCNPIYAFVGEREY 311

Db 256 WTPFNVAIILSSYSLGNCDSKSHLDVMAIYEVAYSHCCNPIYAFVGEREY 314  
QY 312 LRHEFH 317  
Db 315 ---LFH 317

## RESULT 10

A57160  
chemokine (C-C) receptor 4 - human  
N:Alternate names: C-C-CCR-4  
C:Species: Homo sapiens (man)  
C:Date: 10-Nov-1995 #sequence, revision 10-Nov-1995 #text, change 21-Jul-2000  
C:Accession: A57160  
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.  
J. Biol. Chem. 270, 19495-19500, 1995  
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor  
A:Reference number: A57160; MUID:95370289; PMID:7642634  
A:Accession: A57160  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-360 <POK>  
C:Cross-references: GB:X85740; NID:91370103; PIDN:CAA59743.1; PID:9711452  
A:Note: source clone K5-5  
C:Genetics:  
A:Gene: GDB:CMKBR4  
A:Cross-references: GDB:677463  
A:Map position: 3p21-3p21  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p  
F:40-65/Domain: transmembrane #status predicted <TM1>  
F:76-97/Domain: transmembrane #status predicted <TM2>  
F:112-133/Domain: transmembrane #status predicted <TM3>  
F:151-175/Domain: transmembrane #status predicted <TM4>  
F:208-226/Domain: transmembrane #status predicted <TM5>  
F:243-264/Domain: transmembrane #status predicted <TM6>  
F:291-308/Domain: transmembrane #status predicted <TM7>  
F:29-276/110-187/Disulfide bonds: #status predicted  
F:172-350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predi  
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predi  
F:183/Binding site: carbohydrate (Asn) (covalent) (by protein kinase C) #status predi  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predi

Query Match 43.3%; Score 803.5; DB 2; Length 360;  
Best Local Similarity 46.2%; Pred. No. 2, 56-60;  
Matches 163; Conservative 68; Mismatches 113; Indels 9; Gaps 7;

QY 3 TSLDVERFGTTSY-YDVGGLCEKADRALMAQFVPPYLSLVFTVGLGNVVMILIK 61  
Db 9 TFLD--ESIVSNYLYESIPRCCKEIKARGELPLPYLSLVFTVGLGNVVMILIK 66  
QY 62 YRLRIMNITLNMALISDLFLVTLPMVHVRGNHNVFGHCKLLSGFHTGLYSIEI 121  
Db 67 YRLRIMNITLNMALISDLFLVTLPMVHVRGNHNVFGHCKLLSGFHTGLYSIEI 125  
QY 122 FEIILITIDRIYLAIVHAFALRARTVGTGVTISVTWGLAVLAALPEFIYETEELFEET 181  
Db 126 FEVHMSIDRIYLAIVHAFALRARTVGTGVTISVTWGLAVLAALPEFIYETEELFEET 185  
QY 182 LCSALYEDTVYVSRNHEHTLMTFICLVPLLVMAICTGTGIIKTLRCPKSKKKAIRL 241  
Db 186 YCKTYSINST-TWVLSLSLEINILGLVPIGLIMFCYSMIIRTLQHCNKKRAVKMI 244  
QY 242 FVMAVPEIEMTPYNAIILSSYSLGNCDSKSHLDVMAIYEVAYSHCCNPIY 301  
Db 245 FAVVAVLEGFEMTPYNAIILSSYSLGNCDSKSHLDVMAIYEVAYSHCCNPIY 304  
QY 302 AVGEREYKRYLRHFEH--RHLMLHGRYIFLPSEKLETSVSPSTAEPEL 351  
Db 305 FFLGKRYKRYLQLEKTCRGLFV-LCQYGLLQIYSADTPSSYQSTIMNDL 356

## RESULT 11

JC4587  
 chemokine (C-C) receptor 4 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000  
 C:Accession: J04587  
 R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996  
 A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to  
 A:Reference number: J04587; MUID:96136324; PMID:8573157  
 A:Accession: J04587  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <HO>  
 A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CA062372.1; PID:g1167852  
 A:Experimental source: thymus  
 C:Genetics:  
 A:Gene: cc\_ckt-4  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus  
 F:2,183,194/Binding site: carbohydrate (Aan) (covalent) #status predicted  
 F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred  
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 42.1%; Score 780.5; DB 2; Length 360;  
 Best Local Similarity 45.0%; Pred. No. 2,2e-58;  
 Matches 154; Conservative 71; Mismatches 110; Indels 7; Gaps 5;

```

OY 2 TTSDIVTFTGTSYDDVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMILIK 61
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 9 TTQDETVA--YNSYFYFESMPKRCQEGIKARCEVPLPLYSLVFLGFGNSVVLVFK 66
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 62 YRLRLNINILANLADLFLVLPFMHIVYRHNHNVFGHGMCKLISGEFTHTLSRI 121
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 67 YKRLKSMIDVLLNLAIDLFLVLSLPTMGTYA-ADQNVFGIGLKIKTYSMTLVGFSGI 125
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 122 FFILITDRYLAIVHAFALRAKTVTEGVITSTVWGLAVLALPEFLFYETEELFEET 181
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 126 FFIMLSIDRYLAIVHAFSLKARLTVGVITSLTWGVAVAFASLPGLEFSCVTEHNT 185
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 182 LCSALPDPDYVSRHFTLMTIFCLVPLPLVNAICTGIIKTILRCPKSKRYAIRLI 241
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 186 YCKTQYVSNST-TWKLVSLSLEINVLGILPIGLIMFWYSMTIRLQHCNKKRAVIMI 244
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 242 FVMAVFFIETFPYNAVALISSYOSILFNGDCERSKHLDMVLVTEVAISHCCNPIY 301
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 245 FGVVVLFGFTFPYNAVALFETIVELEVLQDCTLERIDYAIQATETGFIHCCNPIY 304
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 302 AFVGERFRKYLRHFFH--RHLLMLGRYIPELPSEKLERTSS 341
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 305 FFLGEEKFRKYITQLFRFCRGLV-LCKHCDFLQVYSADMS 345
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

RESULT 12  
 158186  
 Probable G protein-coupled receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jul-2000  
 C:Accession: 158186  
 R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.  
 Neurosci. Lett. 169, 85-89, 1994  
 A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and h  
 A:Reference number: 158186; MUID:94323113; PMID:8047298  
 A:Accession: 158186  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <RES>  
 A:Cross-references: EMBL:U04808; NID:g2558635; PIDN:AA087093.1; PID:g439861  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor

Query Match 38.3%; Score 710.5; DB 2; Length 354;  
 Best Local Similarity 42.4%; Pred. NO. 1.7e-52;  
 Matches 146; Conservative 64; Mismatches 123; Indels 11; Gaps 3;

```

OY 17 YDDVGLCEKADTRALMAQFVPLYSLVFTVGLGNVVMILIKYRLRIMFNITLNL 76
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 15 YDDSAEACVGLDIVAFGTIFLSFYSLVFTFGVNLVLAALTNRSKRSSTDITLNL 74
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 77 AISDLFLVLTLPFMHIVYRHNHNVFGHGMCKLISGEFTHTLSRI 136
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 75 AISDLFLVLTLPFMHIVYRHNHNVFGHGMCKLISGEFTHTLSRI 133
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 137 HAFVALRARTVTEGVITSTVWGLAVLALPEFLFYETEELFEETLSALYEDDYVSR 196
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 134 LAANSNNNTVHGVTISIGVAAALVAPSPFMFKR----KNECLADIEVLOETNP 189
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 197 HFHTLMTIFCLVPLPLVNAICTGIIKTILRCPKSKRYAIRLI 256
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 190 VLRNSEVNILGVLPLILMSFCYFRIVRFLSCNKKRAIRLILVYVVEFLFTPN 249
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 257 VALISSYOSILFNGDCERSKHLDMVLVTEVAISHCCNPIYAFVGERFRKYLRHFF 316
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 250 IYIFLETLEFYNFPPSCGKRLRMALSTETVAVSHCCNLPFIYAFAGEKFRYRLILY 309
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 317 HRHLLMLGRYIPELPSEKLERT-----SSVSPSTAEPDELSTV 354
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 310 NKCLAVLCGRPVHAGFSTESQRSRODSILSLTHYTSBGSGSL 353
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

RESULT 13  
 JC5067  
 G protein-coupled receptor CKR-11 - human  
 N:Alternate names: chemokine receptor-11-like protein TER1; GPR-CY6  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jul-2000  
 R:Zabellios, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.  
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996  
 A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-11k  
 A:Reference number: JC5067; MUID:97040707; PMID:8886020  
 A:Accession: JC5067  
 A:Molecule type: DNA  
 A:Residues: 1-355 <ZAB>  
 A:Cross-references: EMBL:Z79782; NID:g1668735; PIDN:CA802142.1; PID:g1668736  
 R:Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.  
 Submitted to the EMBL Data Library, June 1996  
 A:Reference number: H01714  
 A:Accession: G02776  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-355 <NAP>  
 A:Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979  
 R:Bonner, T.I.  
 Submitted to the EMBL Data Library, January 1996  
 A:Reference number: H01154  
 A:Accession: G02387  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-355 <BON>  
 A:Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057  
 C:Comment: This protein belongs to the family of beta chemokine receptors.  
 A:Gene: GDB:CMKBR8; CMKBR2; TER1; CKR-11  
 A:Cross-references: GDB:6053733; OMIM:601394  
 A:Map position: 3p21-3p21  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; transmembrane protein  
 F:36-63/Domain: transmembrane #status predicted <TM1>  
 F:73-94/Domain: transmembrane #status predicted <TM2>  
 F:108-129/Domain: transmembrane #status predicted <TM3>  
 F:147-171/Domain: transmembrane #status predicted <TM4>  
 F:200-222/Domain: transmembrane #status predicted <TM5>  
 F:239-260/Domain: transmembrane #status predicted <TM6>  
 F:281-304/Domain: transmembrane #status predicted <TM7>

Query Match 37.4%; Score 692.5; DB 2; Length 355;

Best Local Similarity 39.3%; Pred. No. 5.7e-51;  
Matches 137; Conservative 75; Mismatches 120; Indels 17; Gaps 7

Oy	1	MTSLSDFEETGETTSYUDV-GLKE----	KADTRALMOQFPEKLSVETGILLGVV	55
Db	1	MDYTLDLSTVTVTDYVDPDIFSSPCDAELIQNGKLLAVF-----	YCLLEFVETLGNLSV	56
Oy	56	VMILIKYRLRIMINITYLNLALISDLLEPLVLPFWIHVYRGHNWFGHGKMLSGPYHT		115
Db	57	ILVAVCCMKRSTITVYVLLNLALISDLLEFSSPEFYVYLL-DQWVGWVCKRVSQGYXI		115
Oy	116	GLYSEIFPIILTDIRLAYIVAHVAFALRATVTPGVITSIVMGVLVALPEPIFETE		175
Db	116	GFYSMEFPIILMSVDRIYLAHVAVALKRTRIRMGCTTCLAVLWLTAIMATPIPLVETQVA		175
Oy	176	ELFEETLCSALYPEDTVYSWRHPRHTRMTIFCLVLPDLVMAICVYTGIIKTLPQPSKRY		235
Db	176	SEDGVLCQSYFYNQDTL-KMKLETFNKNMILGILPIETFMFCYIKILHQLKCOHNKTY		234
Oy	236	KAIRLPIVMAVFEFMPYPYNAIILSSVOSILFGNDCKSRHLIDVLMLETVIAYASHC		295
Db	235	KAIRVLIVIASLLEFWPFNVVLPETLSHSMHIDGCSISQQLYATHTETIISFPHCC		294
Oy	236	MNPVYIAVGEKFRKYLRIHFHR--HLMHLGRYPIPLPSKELEKTPSS		341
Db	235	VNPVYIAVGEKEFKHLEIFQKSCSQIDINRYGRQ--MPRESCSSSS		340

RESULT 14

JC4304 orphan G protein-coupled receptor - human  
 N:Alternate names: V28 protein  
 C:Species: Homo sapiens (man)  
 C>Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 19-May-2000  
 C:Accession: JC4304  
 R:Report: C.J.; Schweikart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.  
 Gene 163, 295-299, 1995  
 A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to  
 A:Reference number: JC4304; MIMD:96011651; PMID:7590284  
 A:Accession: JC4304

A: Molecule type: mRNA  
A: Residues: 1-355 <RAP>  
A: Cross-references: GB:U20350; NID:g665580; PID:AA91783.1; PID:g665581  
A: Experimental source: peripheral blood mononuclear cell  
C: Comment: This protein is a cell-surface receptor which recognizes extracellular signals  
C: Comment: This protein is a key regulator of many immune and homeostatic responses, and  
C: Genetics:  
A: Gene: V28  
A: Map position: 3pter-p21  
C: Superfamily: vertebrate rhodopsin  
C: Keywords: G protein-coupled receptor; lymphokine; transmembrane protein  
F: 35-57/Domain: transmembrane #status predicted <TM1>  
F: 66-88/Domain: transmembrane #status predicted <TM2>  
F: 104-115/Domain: transmembrane #status predicted <TM3>  
F: 146-165/Domain: transmembrane #status predicted <TM4>  
F: 197-217/Domain: transmembrane #status predicted <TM5>  
F: 230-254/Domain: transmembrane #status predicted <TM6>  
F: 275-296/Domain: transmembrane #status predicted <TM7>

Query Match	36.9%	Score 684	DB 2	Length 355
Best Local Similarity	42.9%	Pred. No. 3e-50		
Matches 144	Conservative 59	Mismatches 117	Indels 16	Gaps 7

  

QY	17	YDDVCLLEKADPTRLAMQFVPPPLSLVFTTVELGNNVVMILIKRRLRIMNTIYLM	76
DB	14	YDILAEACYIGDIVVGFVETLSIFPSVFAIGLVMLVAFALNSKPKRSVDIYLM	73
QY	77	AISDLLFLVLTLPFWIHY---RG-HNMYGHGMCKLISFYHTGLSELPFIILITDRY	132
DB	74	ALSDLLFVATLEPFWTHLINEKGLHN----AMCKFTTAEFFIGFGSIFFTIVISIDRY	128
QY	133	LAIVAVAFALRKARYTFCGYTISIVWGLAVLALPFIYETHEBELFEERLCSALPEDRY	192

```

Dh 129 LAIVLAANSNNNTVOGHVITISLGYMAAAILVAARQFME--TKQ--KENELGDYPRVLQ 164
Oy 193 YSMRHEHTLTMTIECLVLPDLVMAICYGIIKTLTLPDCKKKRYAIRLIEVIAVFEIEM 252
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dh 185 EIVPVLARNETNFIQELTLPILLINSXYCFERRIIQTLFSCNHHKRAAKIKLIIIVLVPELFM 244
Oy 253 TPVNVAILLSYGSIILFGDNCERSKHLDLYMLVTEVIAVYSHCCAMPYIYAFVGRFRKYL 312
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dh 245 TPVNVMIETETKLVDYFPSCDRMDLRIALSVTETVAFSHCICPLIYAFAGGERFRYL 304
Oy 313 RHEFHRILMHILGR--YIPLPSE-KLERTSVSPS 345
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dh 305 YHLXGKCLAVLCGRVHYDFSSSESQSRSHGSVLSS 340

```

### RESULT 15

chemokine receptor - human  
C.Species: Homo sapiens (man)  
C.Date: 16-Jul-1999 #sequence\_reviston 16-Jul-1999 #text\_change 21-Jul-2000  
C.Accession: J05942  
R.Fan, P., Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.  
Biochem. Biophys. Res. Commun. 243, 264-286, 1998  
A.Title: Cloning and characterization of a novel human chemokine receptor.  
A.Reference number: J05942; PMID:9813902; PMID:9473515  
A.Accession: J05942  
A.Status: preliminary  
A.Molecule type: DNA  
A.Residues: 1-344 <FAN>  
A.Cross-References: GB:U97123; NID:q2897070; PIDN:MAC39595.1; PID:q2897071  
C.Superfamily: vertebrate rhodopsin

Query Match	35.6%	Score 659.5;	DB 2,	Length 344;
Best Local Similarity	42.1%	Pred No. 3.3e-48;		
Matches 141; Conservative	59;	Mismatches 108;	Indels 27;	Gaps 8

```

0Y      24 CERADPFLMAAOVPPPLYSIVFTVGLGWNVVMILLIKRRLRITNTIYLNTAISDLF  83
Db      28 CDKDAQALSAOIVPSPISCSAVFVIGLIDMLVLLIVLYKGKREMYNTLNTLVNSICF  87
0Y      84 LVTLPEWIVHVRGHNWVGHGCKKLISGFEYHGLYSEIFFIILLIDREYLAIVHA--VFA  141
Db      88 LILIPFMAH-----AGDPMCKILIGLEWGLISETFPNCILLVQRIVLFLKGNFES  140
0Y      142 LRATVYFGVITSIVMWGLAVLAALPEEIFEETEELEETIC---SALYEDPTVYSWRH  197
Db      141 AR-RRVYCGITISVLMYATLAILATPEIYVYVYRQEDQKYKCAFSRTFFLPADETF--WKH  198
0Y      198 FHTLRMTIFCLVPLPLVMAICYGTIGLITLLRQPSKKYKAIRLIFVIAVEFIMTPYNV  257
Db      199 FLTLKNNISVLYPLPIFFFLYVQMKTLRF--REGQSLFLFVPAIVMVLMMAPNYI  256
0Y      258 AILISQSITLIFGNDCEBSKHLIDVMLVLEVAIYSHCCNRPYIYAFVGERRRKTLRHFH  317
Db      257 AFPLSTPEKHFSLSDCKSSYNLDRSHVIRKLATTHCCINPLVYAFPLDGTESKYLCRCF-  315
0Y      318 RHLMLHGRIYPIPLPSKLELRNSSVSPSTAADELS  352
Db      316 ----HLRSTNPIDPQGO----SAQTSSEEDPHS  341

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Search completed: June 27, 2003, 18:15:49  
Job time : 41 secs



